Phyre^2

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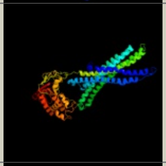
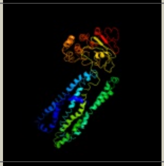
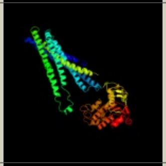
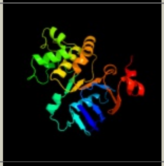
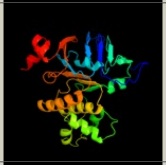
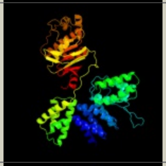
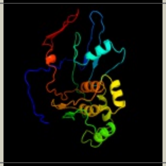
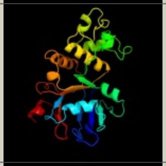
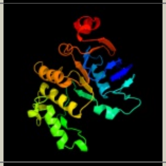
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b5wE_	Alignment		100.0	100	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
2	c2hydB_	Alignment		100.0	34	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
3	c2yl4A_	Alignment		100.0	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10, **PDBTitle:** structure of the human mitochondrial abc transporter, abcb10
4	c3b5xB_	Alignment		100.0	68	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
5	c3g5uB_	Alignment		100.0	31	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
6	c3nhaA_	Alignment		100.0	46	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 6, mitochondrial; **PDBTitle:** nucleotide binding domain of human abcb6 (adp mg bound structure)
7	d3b60a1	Alignment		100.0	95	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
8	d2pmka1	Alignment		100.0	48	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
9	d2hyda1	Alignment		100.0	52	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
10	d1mv5a_	Alignment		100.0	44	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
11	d1jj7a_	Alignment		100.0	41	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like

12	c2cbzA_	Alignment		100.0	32	**PDB header:**transport **Chain:** A: **PDB Molecule:**multidrug resistance-associated protein 1; **PDBTitle:** structure of the human multidrug resistance protein 12 nucleotide binding domain 1
13	c2iw3B_	Alignment		100.0	14	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 3a; **PDBTitle:** elongation factor 3 in complex with adp
14	d1pf4a1	Alignment		100.0	71	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
15	c2r6fA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
16	c2ghiD_	Alignment		100.0	46	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport protein; **PDBTitle:** crystal structure of plasmodium yoelii multidrug resistance2 protein 2
17	c2pzfB_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cystic fibrosis transmembrane conductance regulator; **PDBTitle:** minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
18	c3gd7C_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fusion complex of cystic fibrosis transmembrane **PDBTitle:** crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
19	c2olkD_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
20	d1ji0a_	Alignment		100.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
21	d1xmia_	Alignment	not modelled	100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
22	c3gfoA_	Alignment	not modelled	100.0	25	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**cobalt import atp-binding protein cbio 1; **PDBTitle:** structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
23	c1oxtB_	Alignment	not modelled	100.0	31	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, atp binding protein; **PDBTitle:** crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
24	c2yyzA_	Alignment	not modelled	100.0	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
25	c1z47B_	Alignment	not modelled	100.0	31	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative abc-transporter atp-binding protein; **PDBTitle:** structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
26	d1r0wa_	Alignment	not modelled	100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
27	c3fvqB_	Alignment	not modelled	100.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc; **PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp
28	c2it1B	Alignment	not modelled	100.0	36	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical

						maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
29	d1b0ua_	Alignment	not modelled	100.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
30	d3dhwc1	Alignment	not modelled	100.0	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
31	d3d31a2	Alignment	not modelled	100.0	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
32	c3dhwC_	Alignment	not modelled	100.0	31	**PDB header:**membrane protein/hydrolase **Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn; **PDBTitle:** crystal structure of methionine importer metni
33	d1oxxk2	Alignment	not modelled	100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
34	d1vpla_	Alignment	not modelled	100.0	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
35	d1g2912	Alignment	not modelled	100.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
36	d1g6ha_	Alignment	not modelled	100.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
37	c2d2fA_	Alignment	not modelled	100.0	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
38	c1vciA_	Alignment	not modelled	100.0	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar-binding transport atp-binding protein; **PDBTitle:** crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
39	c2d62A_	Alignment	not modelled	100.0	28	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**multiple sugar-binding transport atp-binding **PDBTitle:** crystal structure of multiple sugar binding transport atp-2 binding protein
40	c1q1bD_	Alignment	not modelled	100.0	30	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**maltose/maltodextrin transport atp-binding protein malk; **PDBTitle:** crystal structure of e. coli malk in the nucleotide-free form
41	d1v43a3	Alignment	not modelled	100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
42	c2yz2B_	Alignment	not modelled	100.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative abc transporter atp-binding protein tm_0222; **PDBTitle:** crystal structure of the abc transporter in the cobalt transport2 system
43	d1l2ta_	Alignment	not modelled	100.0	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
44	c2pcjB_	Alignment	not modelled	100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein-releasing system atp-binding protein lold; **PDBTitle:** crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
45	c3d31B_	Alignment	not modelled	100.0	32	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sulfate/molybdate abc transporter, atp-binding **PDBTitle:** modbc from methanosarcina acetivorans
46	c2nq2C_	Alignment	not modelled	100.0	25	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**hypothetical abc transporter atp-binding protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
47	c2d3wB_	Alignment	not modelled	100.0	22	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**probable atp-dependent transporter sufc; **PDBTitle:** crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
48	d2onka1	Alignment	not modelled	100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
49	c2ihyB_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**abc transporter, atp-binding protein; **PDBTitle:** structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
50	d1l7vc_	Alignment	not modelled	100.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
51	c2pjzA_	Alignment	not modelled	100.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st1066; **PDBTitle:** the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
						PDB header:hydrolase

52	c2ygrD_	Alignment	not modelled	100.0	23	**Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
53	d1sgwa_	Alignment	not modelled	100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
54	c1yqtA_	Alignment	not modelled	100.0	31	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
55	c3ozxA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
56	d3b60a2	Alignment	not modelled	100.0	97	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
57	d2awna2	Alignment	not modelled	100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
58	c3bk7A_	Alignment	not modelled	100.0	28	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
59	c3pihA_	Alignment	not modelled	100.0	27	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
60	d2hyda2	Alignment	not modelled	100.0	18	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
61	c2vf7B_	Alignment	not modelled	100.0	26	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
62	d1pf4a2	Alignment	not modelled	99.9	65	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
63	d1w1wa_	Alignment	not modelled	99.9	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
64	d1cr2a_	Alignment	not modelled	99.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
65	c3tauB_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of a putative guanylate monophosphaste kinase from2 listeria monocytogenes egd-e
66	c2j41A_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
67	c1xexB_	Alignment	not modelled	99.7	24	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
68	c3a4mB_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-seryl-trna(sec) kinase; **PDBTitle:** crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
69	c1f2uD_	Alignment	not modelled	99.6	29	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
70	c1ii8B_	Alignment	not modelled	99.5	34	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
71	d2qy9a2	Alignment	not modelled	99.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
72	c3geiB_	Alignment	not modelled	99.4	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
73	d1ls1a2	Alignment	not modelled	99.3	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
74	d1e69a_	Alignment	not modelled	99.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
75	d1vmaa2	Alignment	not modelled	99.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
76	c3lncB_	Alignment	not modelled	99.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of guanylate kinase from anaplasma2 phagocytophilum
77	d1okkd2	Alignment	not modelled	99.1	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
78	c1u9iA	Alignment	not modelled	99.0	19	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic;

78	c1u9iA_	Alignment	not modelled	99.0	19	**PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
79	d1ye8a1	Alignment	not modelled	98.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
80	c2o5vA_	Alignment	not modelled	98.9	24	**PDB header:**replication/recombination **Chain:** A: **PDB Molecule:**dna replication and repair protein recf; **PDBTitle:** recombination mediator recf
81	c1q57G_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
82	d2i3ba1	Alignment	not modelled	98.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
83	c3auyB_	Alignment	not modelled	98.5	23	**PDB header:**recombination **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** crystal structure of rad50 bound to adp
84	d1np6a_	Alignment	not modelled	98.4	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
85	d1qzxa3	Alignment	not modelled	98.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
86	c2dr3A_	Alignment	not modelled	98.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0273 protein ph0284; **PDBTitle:** crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
87	d1ewqa2	Alignment	not modelled	98.3	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
88	c2w0mA_	Alignment	not modelled	98.2	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
89	c1ewqA_	Alignment	not modelled	98.1	17	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution
90	c2o8dB_	Alignment	not modelled	98.0	18	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh6; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g du mispair
91	c2o8bA_	Alignment	not modelled	98.0	12	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein msh2; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g t mispair
92	c3thxB_	Alignment	not modelled	97.8	17	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh3; **PDBTitle:** human mutsbeta complexed with an idl of 3 bases (loop3) and adp
93	d1nlfa_	Alignment	not modelled	97.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
94	c1wbdA_	Alignment	not modelled	97.7	17	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch
95	c1ewrA_	Alignment	not modelled	97.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of taq muts
96	c2j3eA_	Alignment	not modelled	97.5	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t7i23.11 protein; **PDBTitle:** dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159
97	d1wb9a2	Alignment	not modelled	97.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
98	d1tf7a1	Alignment	not modelled	97.3	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
99	c1wxqA_	Alignment	not modelled	97.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
100	d1tf7a2	Alignment	not modelled	97.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
101	c2gesA_	Alignment	not modelled	97.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase; **PDBTitle:** pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
102	c3pxiB_	Alignment	not modelled	97.2	21	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
103	d1sq5a_	Alignment	not modelled	97.1	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
						Fold:P-loop containing nucleoside triphosphate hydrolases

104	d1odfa_	Alignment	not modelled	97.1	18	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
105	c2recB_	Alignment	not modelled	97.1	18	**PDB header:**helicase **PDB COMPND:**
106	c3bh0A_	Alignment	not modelled	97.0	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
107	c3tqcB_	Alignment	not modelled	97.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
108	c2cvhB_	Alignment	not modelled	97.0	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
109	d1v5wa_	Alignment	not modelled	96.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
110	c3u5zM_	Alignment	not modelled	96.8	20	**PDB header:**dna binding protein/dna **Chain:** M: **PDB Molecule:**dna polymerase accessory protein 44; **PDBTitle:** structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
111	d1zp6a1	Alignment	not modelled	96.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
112	d1n0wa_	Alignment	not modelled	96.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
113	c3ldaA_	Alignment	not modelled	96.8	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
114	c3qg5A_	Alignment	not modelled	96.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rad50; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
115	d2i1qa2	Alignment	not modelled	96.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
116	d1znwa1	Alignment	not modelled	96.7	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
117	c2hcbC_	Alignment	not modelled	96.7	19	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
118	c2plrB_	Alignment	not modelled	96.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thymidylate kinase; **PDBTitle:** crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7
119	c3qkuB_	Alignment	not modelled	96.6	26	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** mre11 rad50 binding domain in complex with rad50 and amp-pnp
120	d1xp8a1	Alignment	not modelled	96.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)